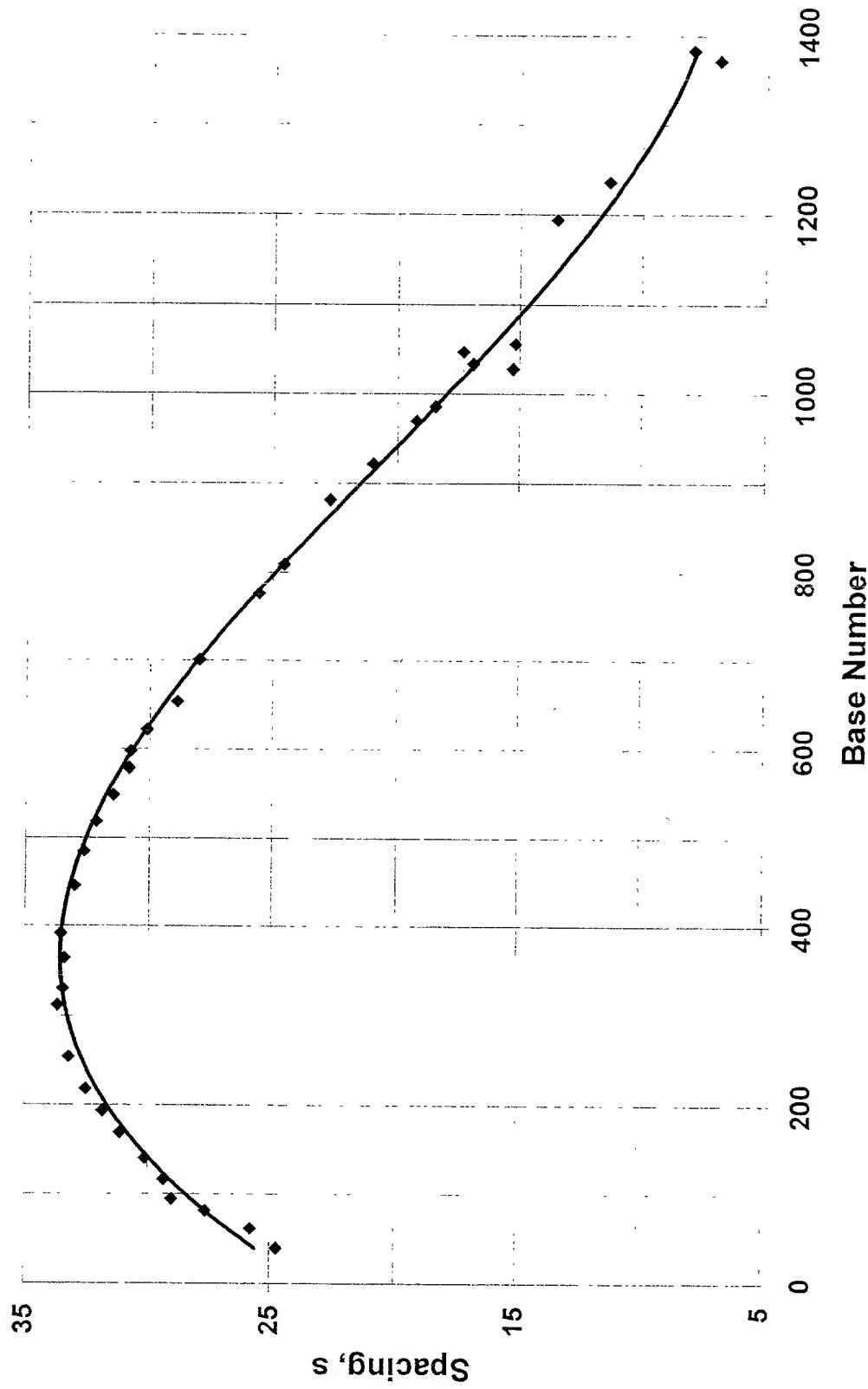


Fig. 1

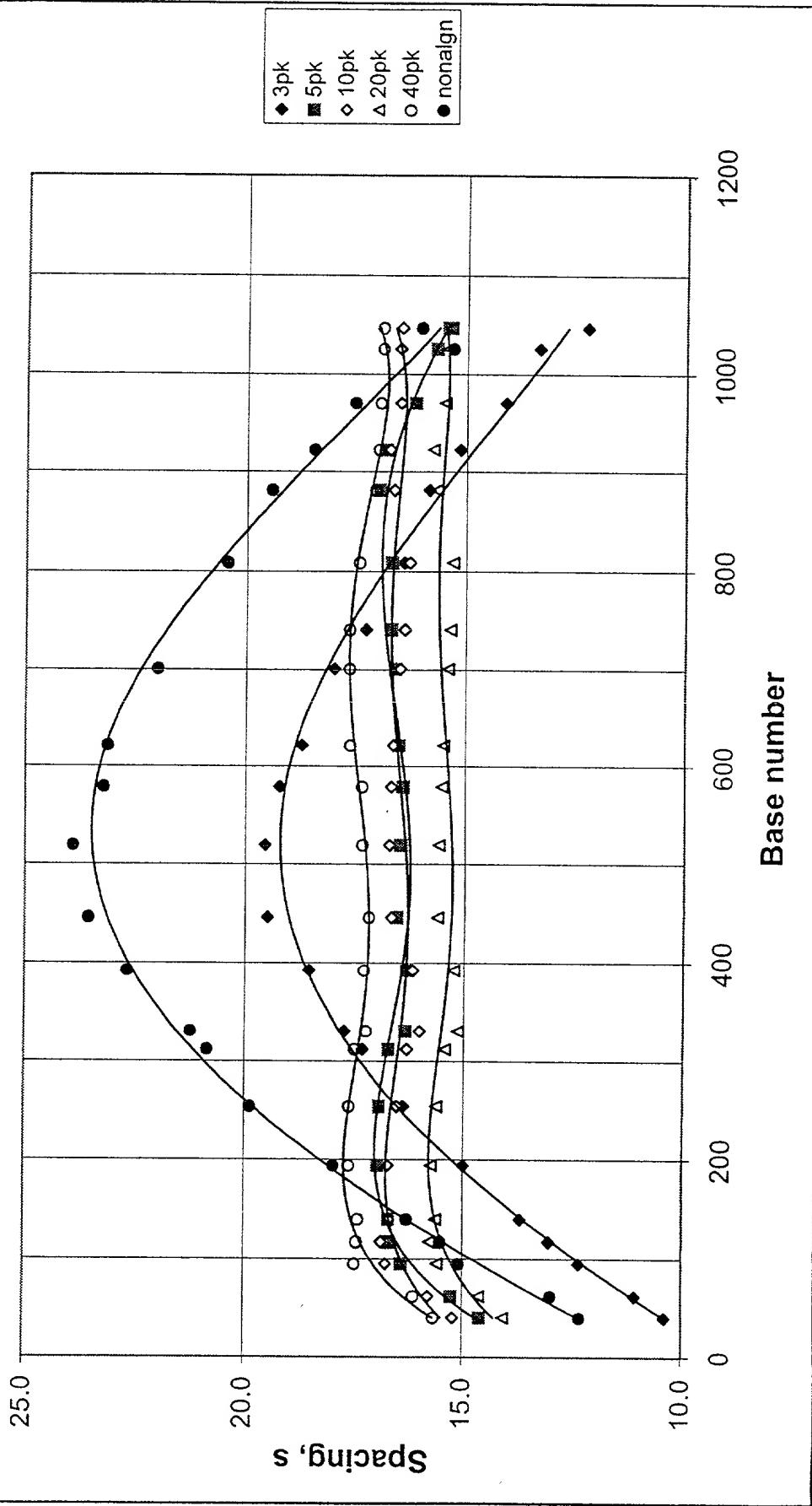
Spacing Between Adjacent Peaks in the Raw Data
(M13, T_s T=6%, 60C, Long Gel)



184

fig. 2

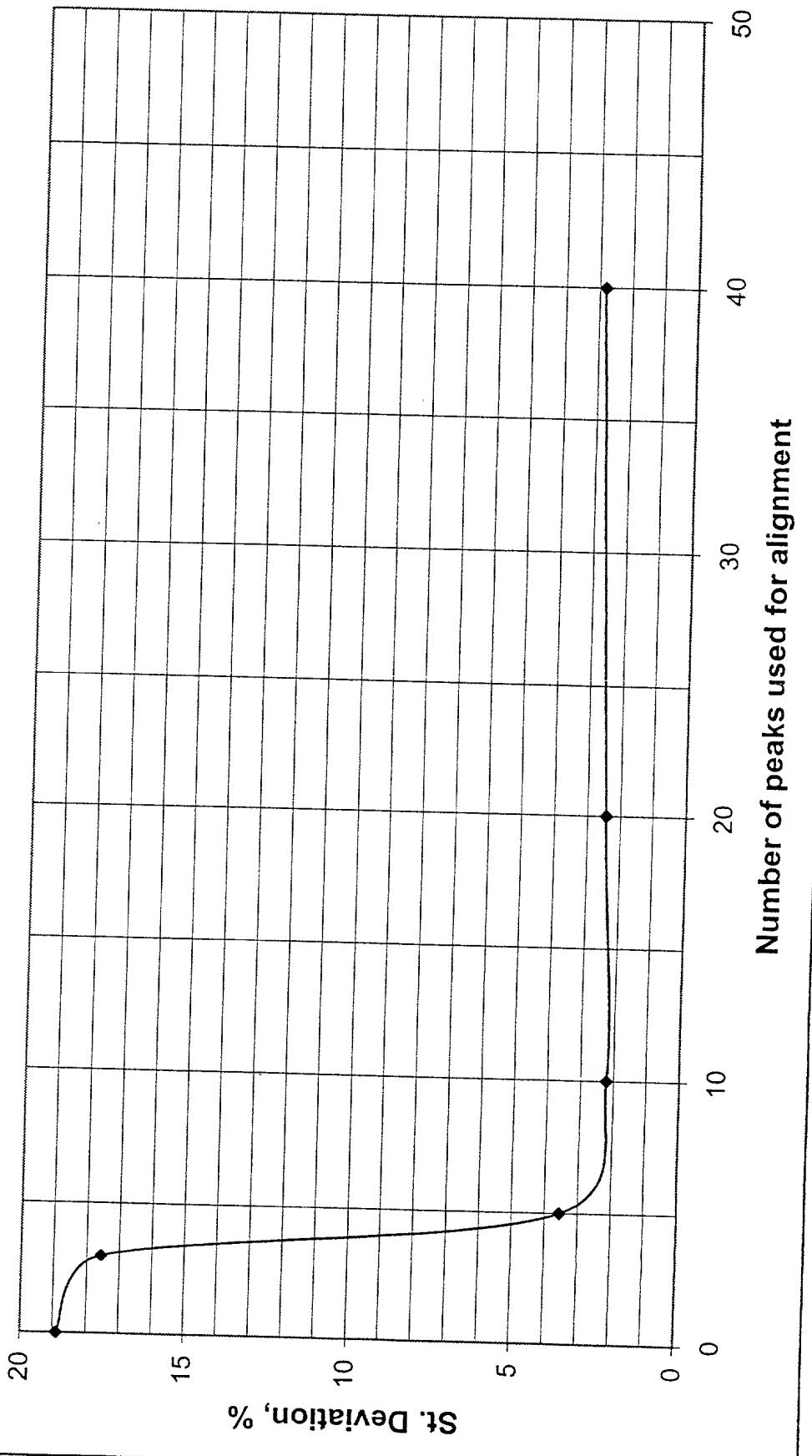
Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data)
(M13, Long Gel, 55C, T=6%)



2/4

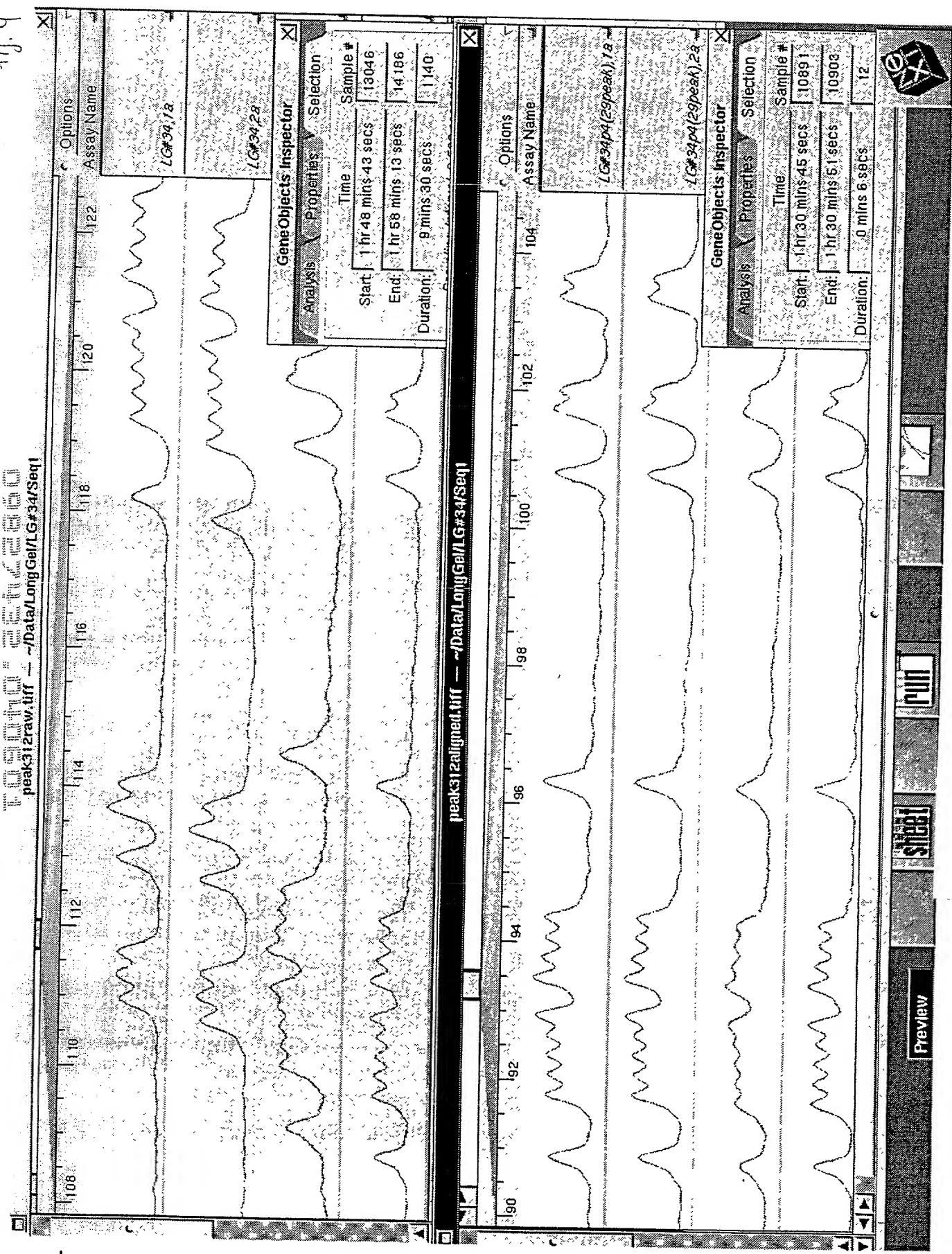
Fig. 3

Standard Deviation (%) of the Spacing Between Adjacent Bases from Average as a Function of Number of Peaks Used as a Reference for Alignment of Raw Data



54

Fig. 4



h 54

Run Time of the BP#1056 in Different Lanes
(after alignment based on 10 peaks)

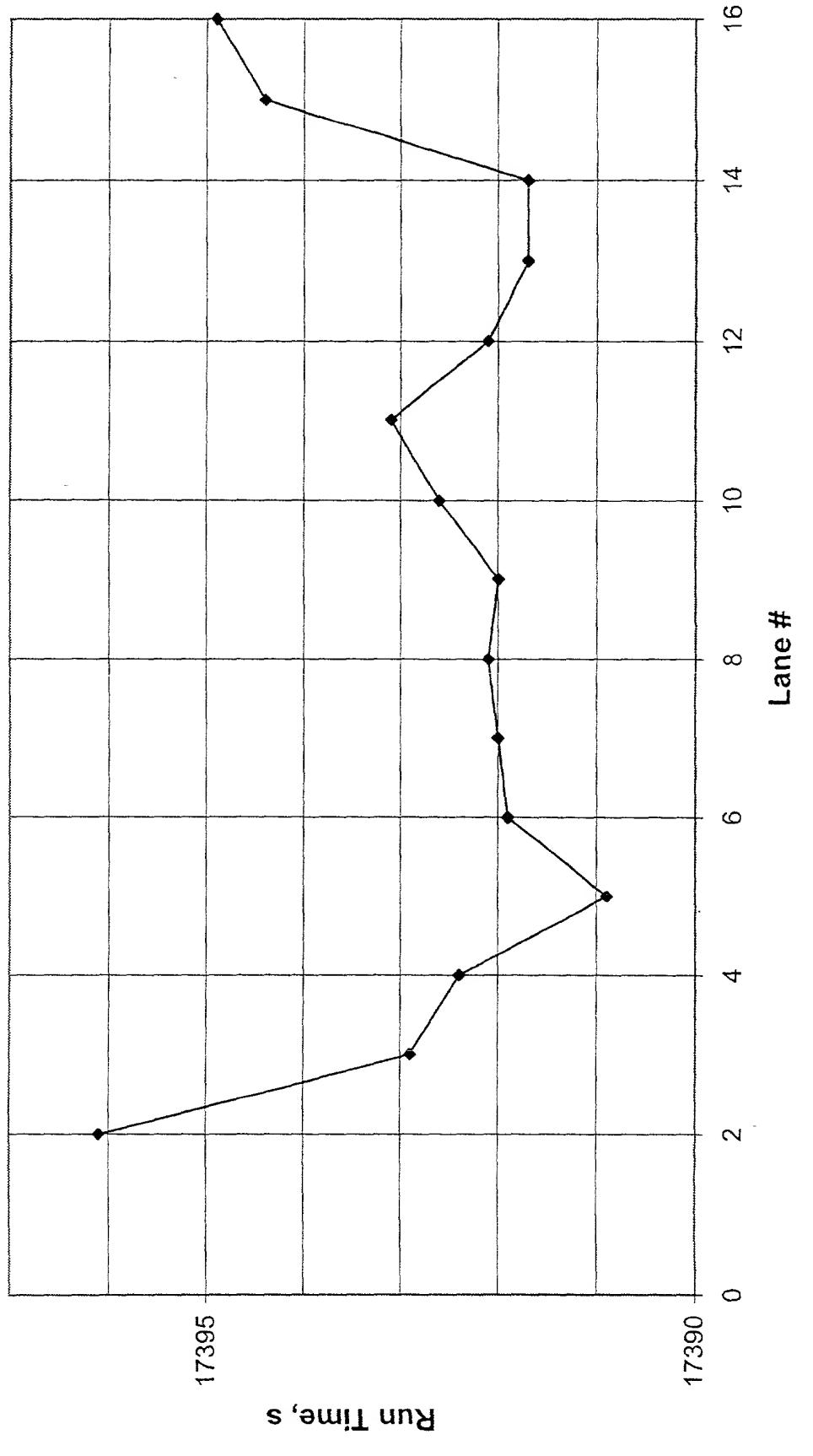
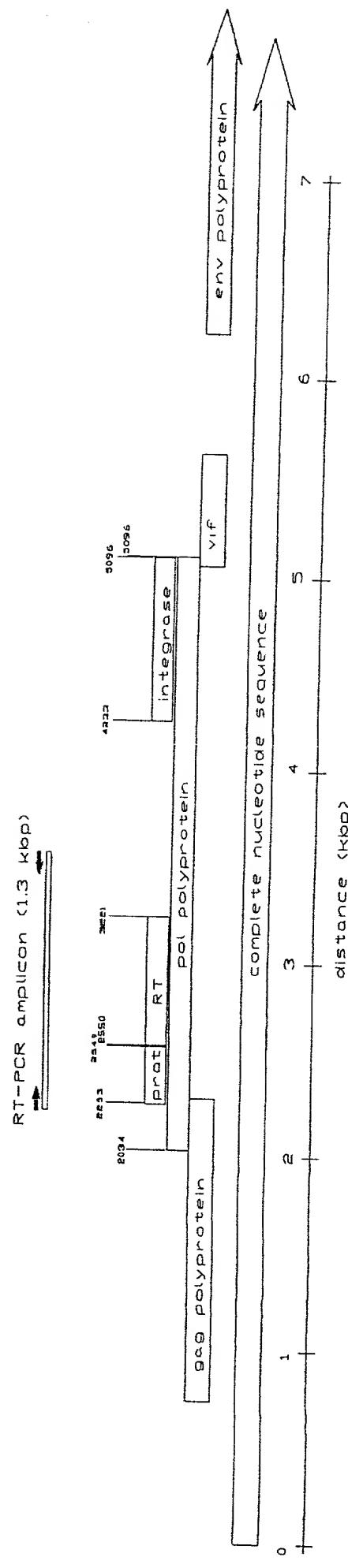
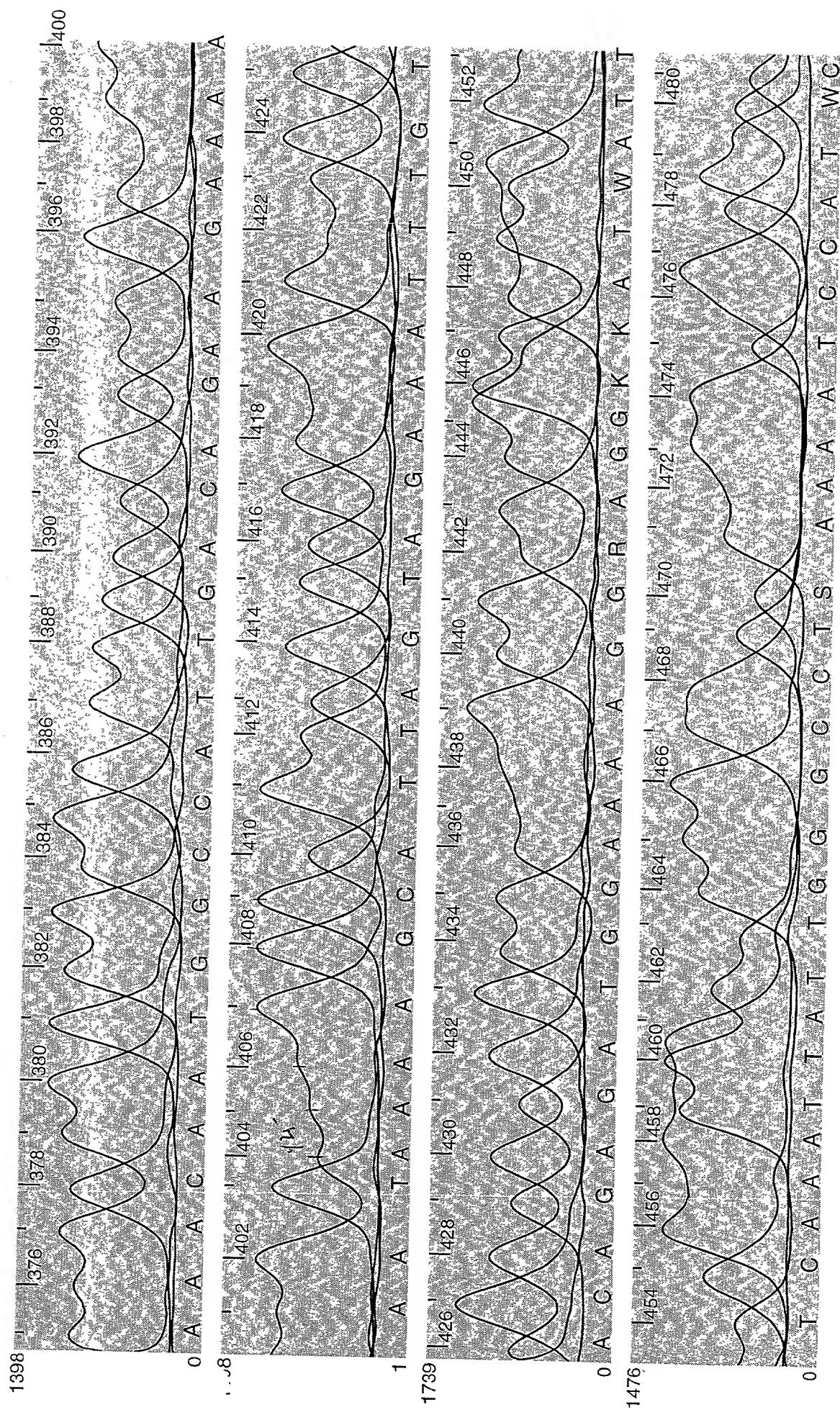
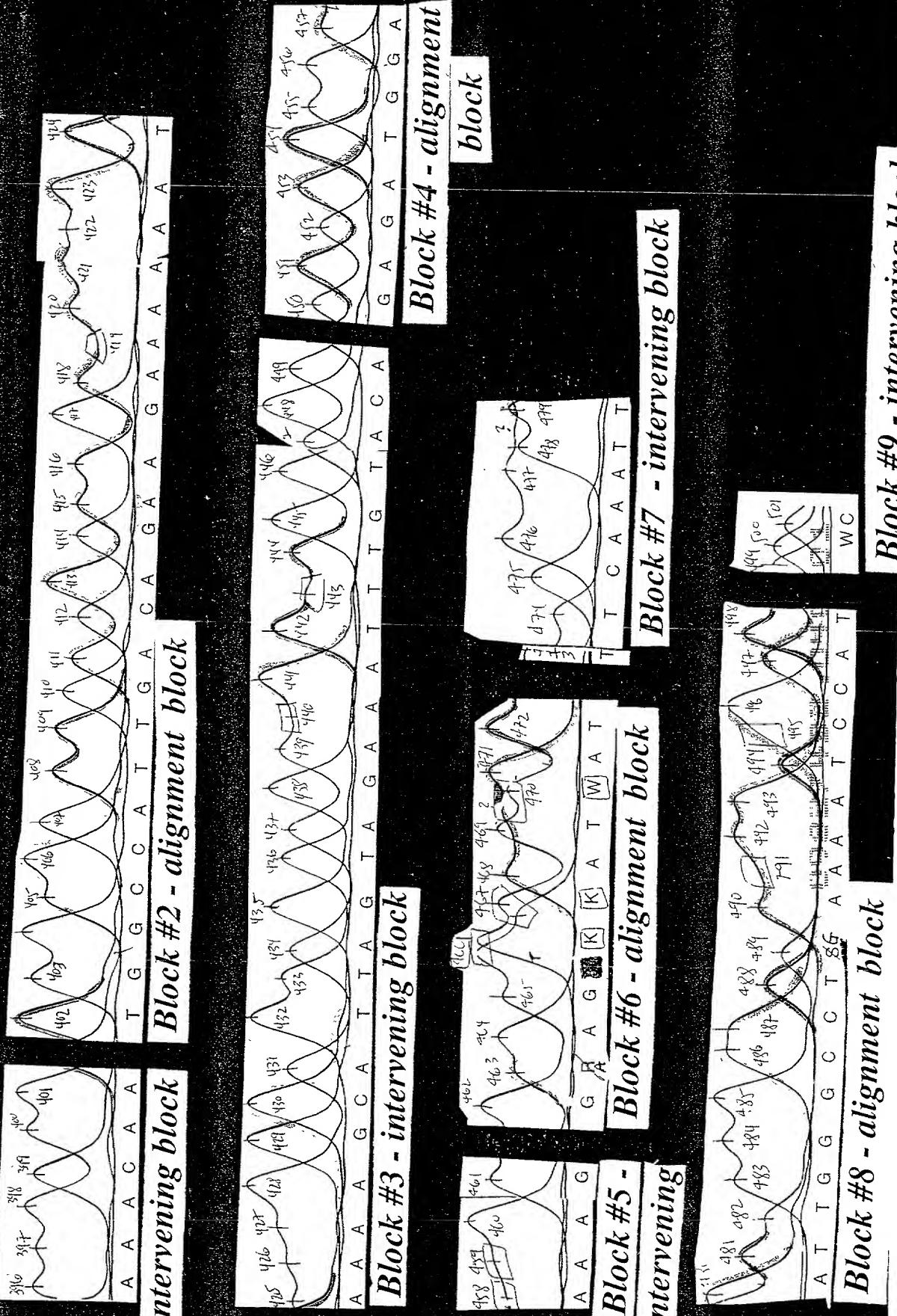


Figure 6



Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc





718

Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc



Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

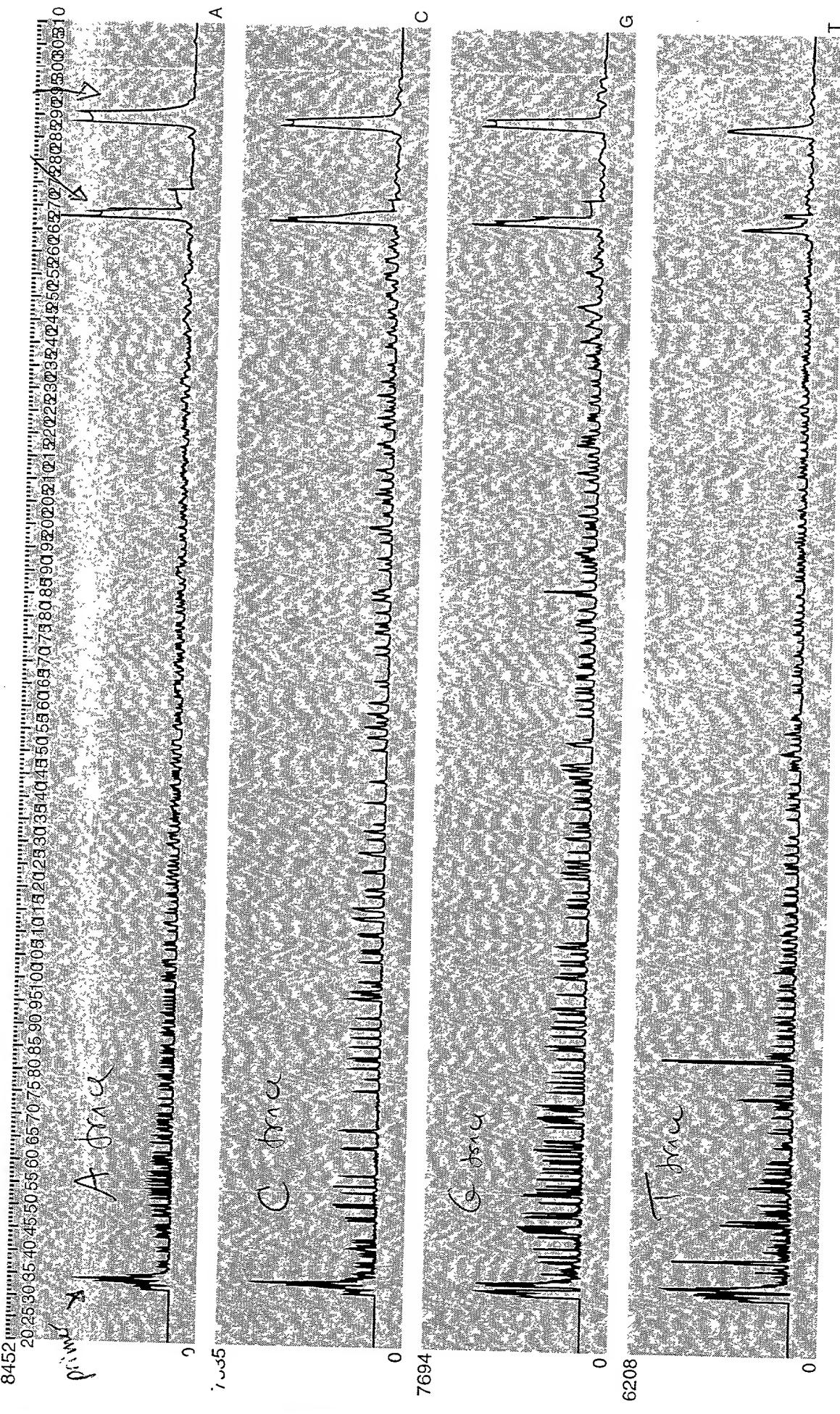


Figure 6A



648 1193 525

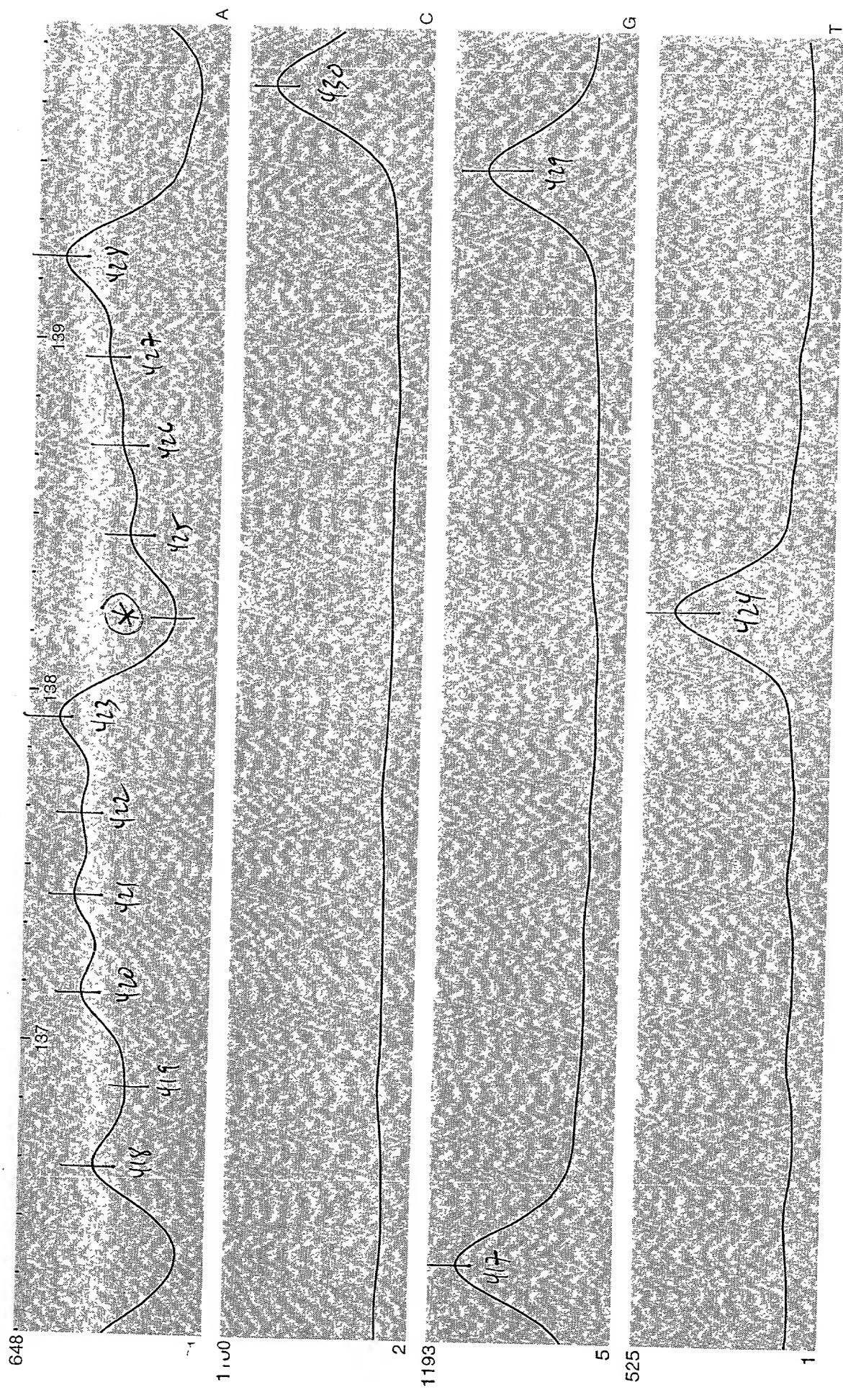


Figure 9B



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Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

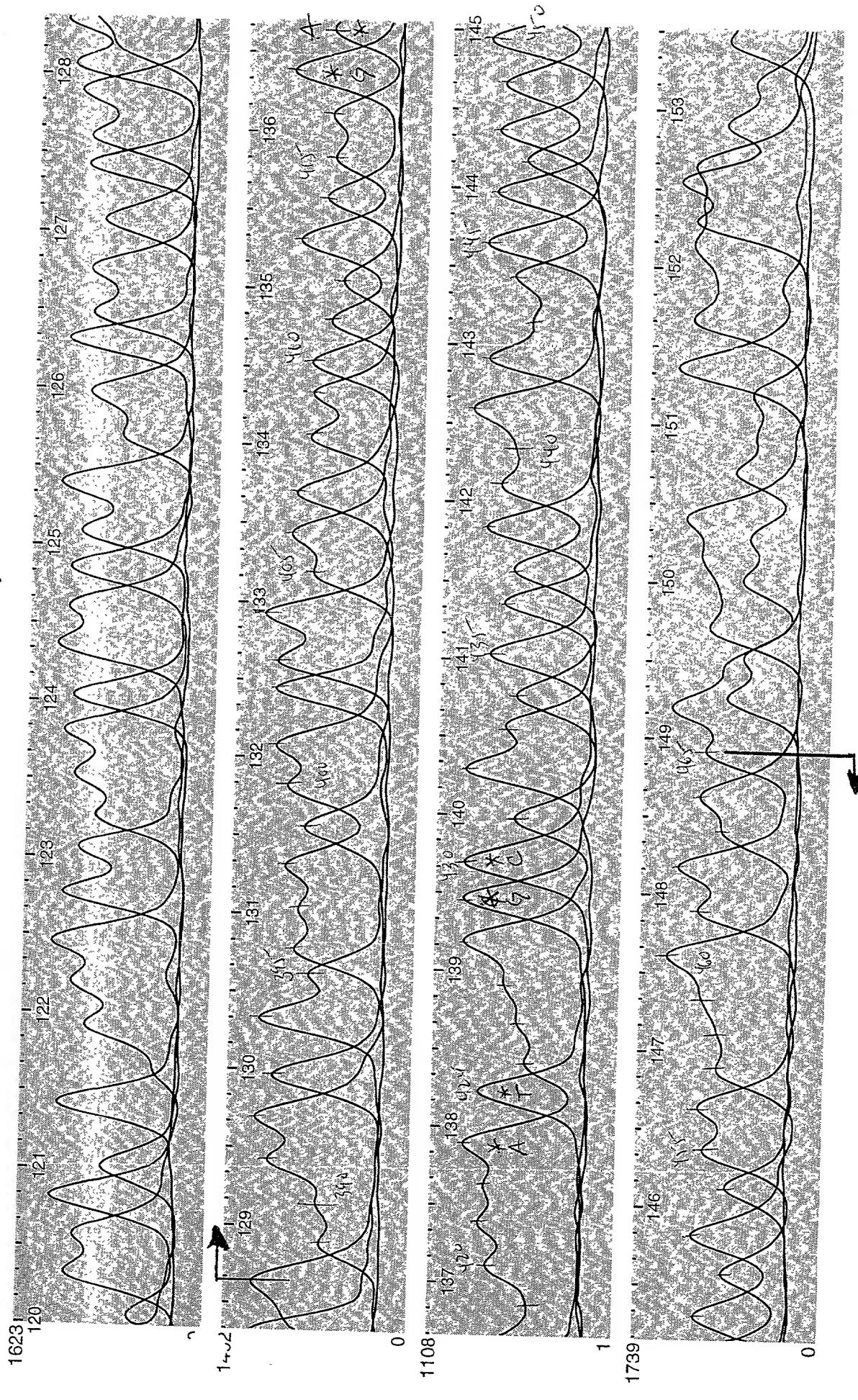


Figure 9

**Deviation of the peak position (in number of bases) from the average
as a function of base number in different traces before alignment**

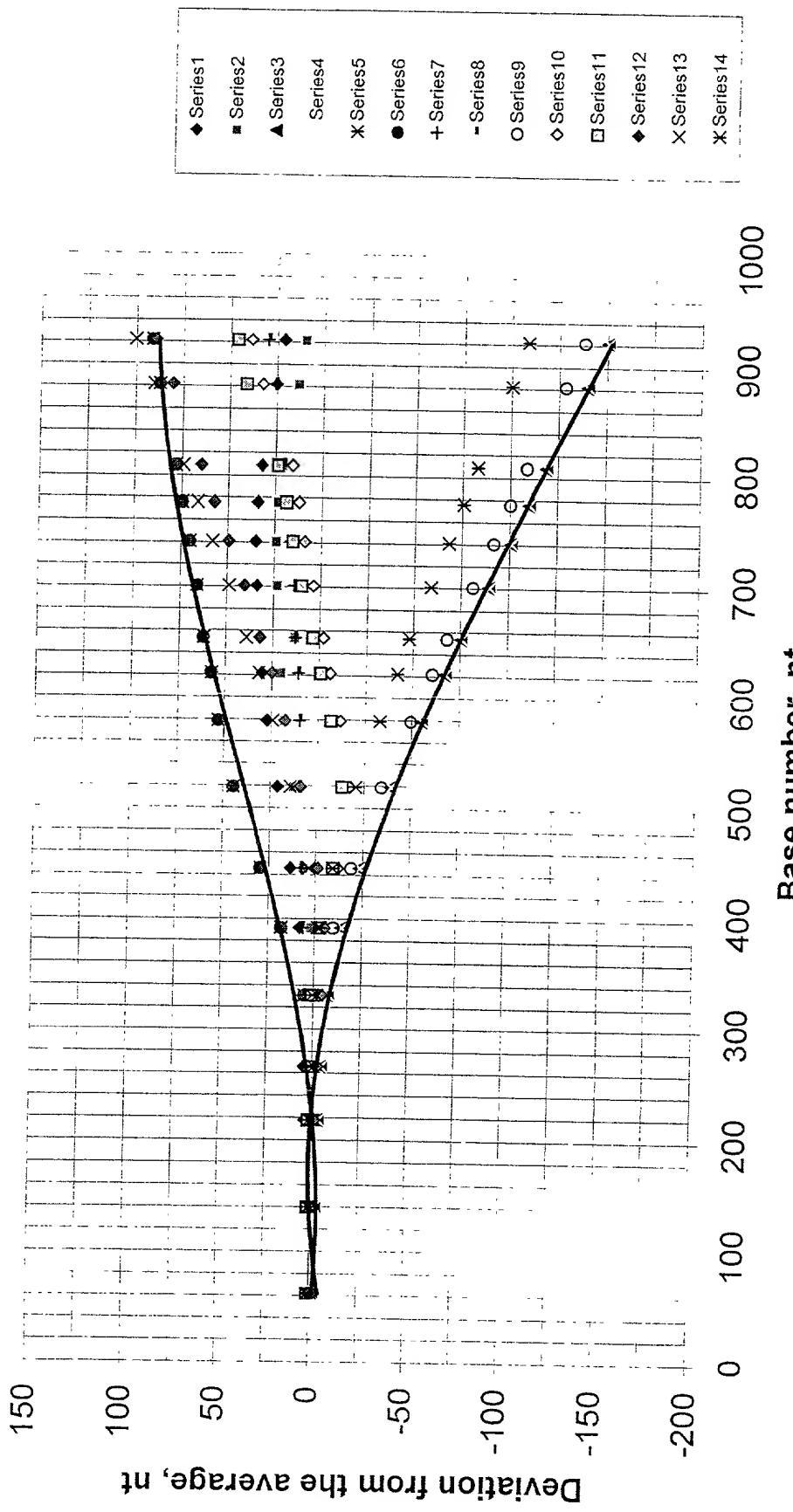


Figure 10

Deviation of the peak position (in number of bases) from the average
as a function of base number in the traces aligned with internal
standards

(long gel, M13, 5-th degree polynomial) 17 Ref. Peaks

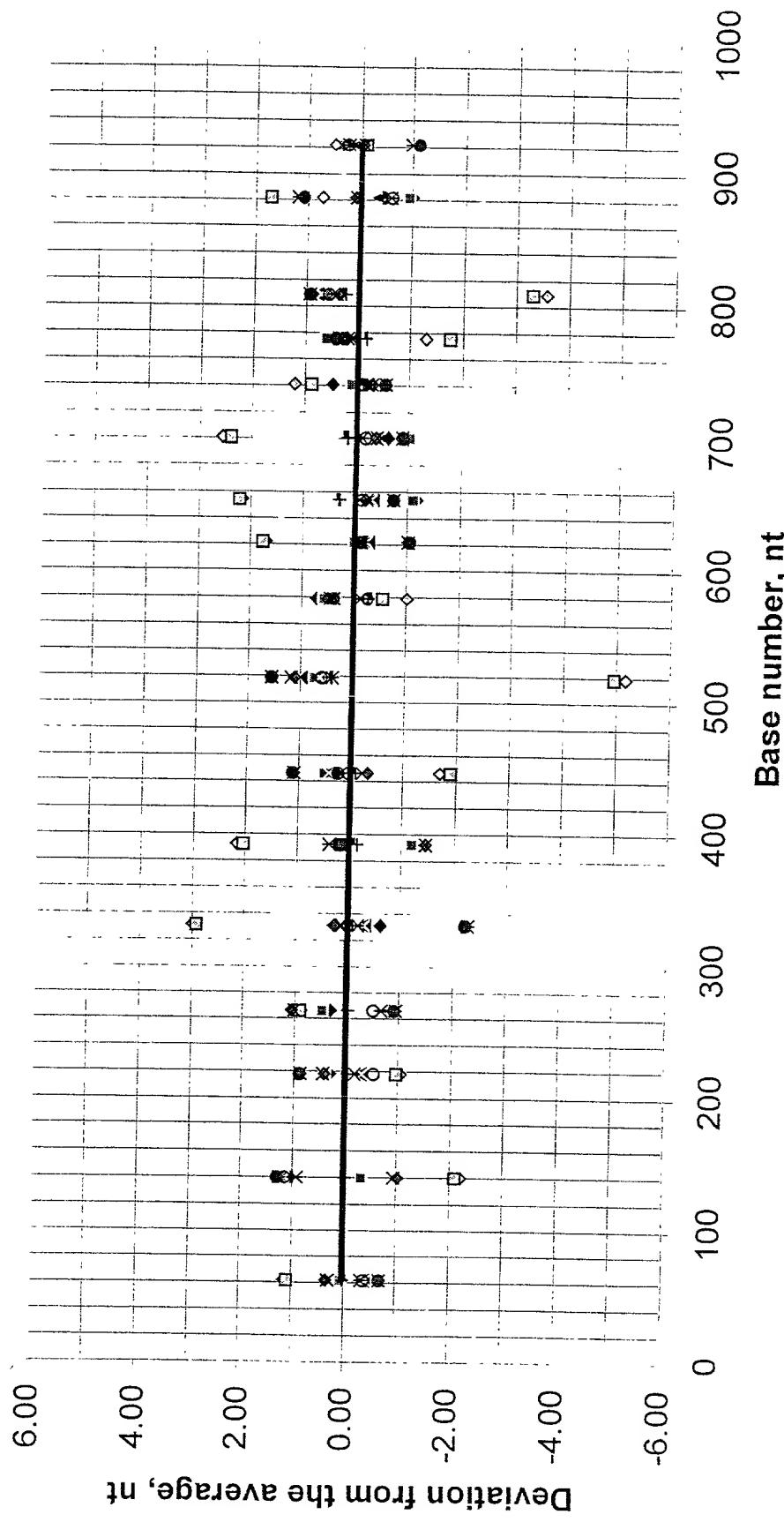


Figure 11

**Deviation of the peak position from the average as a function of base number in the traces aligned with internal standards
(long gel, M13, 6 peaks, 5-th degree polynomial)**

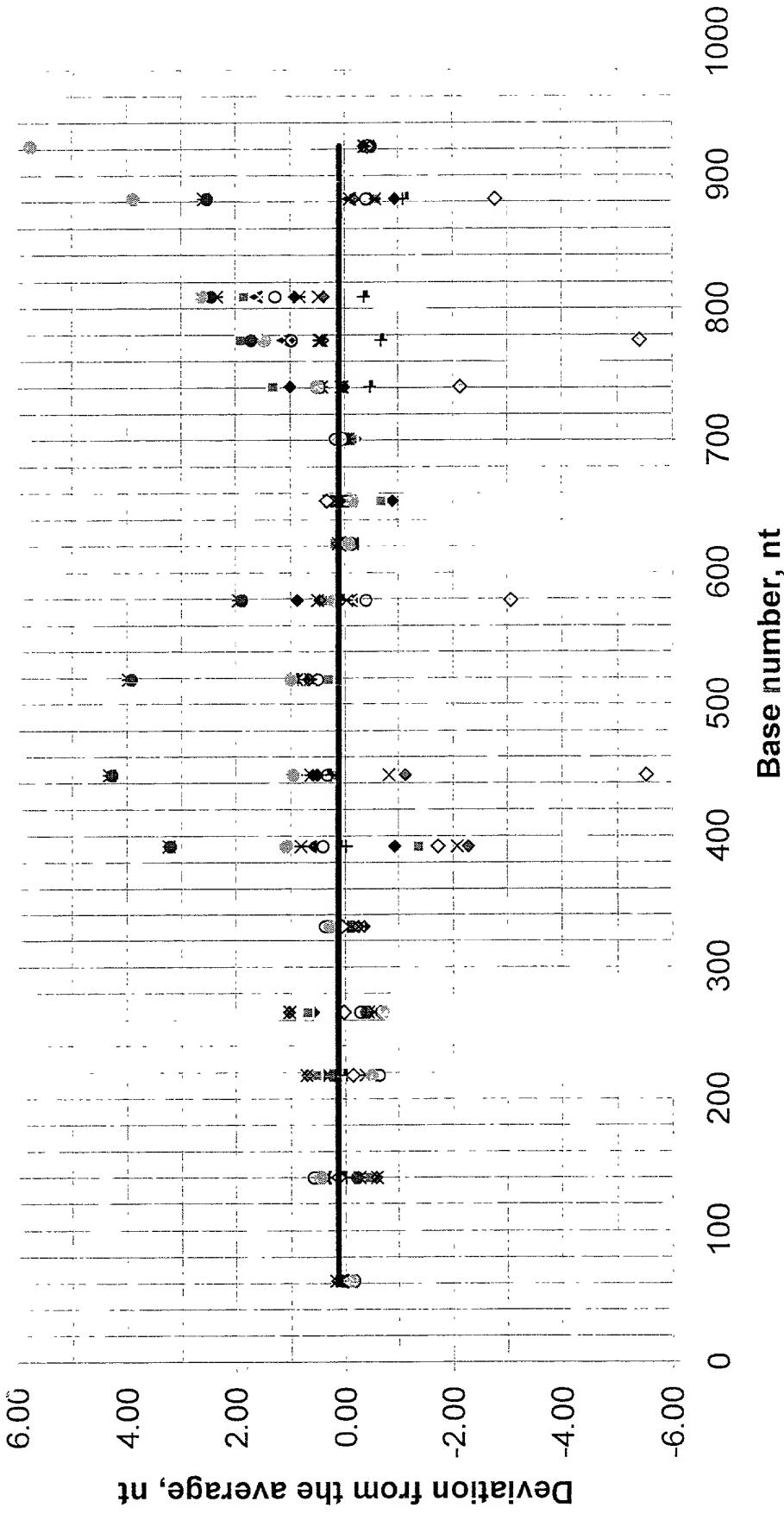


Figure 12